

CRFE

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Access DB# 148326

SEARCH REQUEST FORM

Scientific and Technical Information Center

(STIC)

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 3-21-05
Art Unit: 1635 Phone Number: 202-0765 Serial Number: 09/754,468
Mail Box and Bldg/Room Location: 2D28 Results Format Preferred (circle): PAPER DISK E-MAIL
62018

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: AS Antitumor cell - compo.

Inventors (please provide full names): PATRICK IVERSEN

Earliest Priority Filing Date: 1/4/01

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No: 47 (20 NA)

- Size limit of 100 NT's.

- No size limits

Please search interference +

regular deter base.

Phenol.

SD

STAFF USE ONLY

Type of Search		Vendors and cost where applicable
Searcher: Arnold	NA Sequence (#) 2	STN
Searcher Phone #: 2202	AA Sequence (#)	Dialog
Searcher Location:	Structure (#)	Questel/Orbit
Date Searcher Picked Up: 3/25/05	Bibliographic	Dr. Link
Date Completed: 3/28/05	Litigation	Lexis/Nexis
Searcher Prep & Review Time:	Fulltext	Sequence Systems
clerical Prep Time:	Patent Family	WWW/Internet
Online Time:	Other	Other (specify)

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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 07:42:52 ; Search time 3840 Seconds
(without alignments)
212.620 Million cell updates/sec

Title: US-09-754-468-47

Perfect score: 20

Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 39707814

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 07:27:26 ; Search time 2968 Seconds
(without alignments)
256.498 Million cell updates/sec

Title: US-09-754-468-47

Perfect score: 20
Sequence: 1 gattagcataataaatctc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 675282

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

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8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	79.0	88	1 AA743605	AA743605 oa52b09.i
C 2	15.2	76.0	55	1 AL867656	AL867656 AL867656
C 3	15	75.0	94	8 BH902914	BH902914 SALK 1015
C 4	14.8	74.0	94	9 CG629998	CG629998 OST344683
C 5	14.2	71.0	49	9 BX288153	BX288153 Arabidops
C 6	14.2	71.0	84	2 AW466292	AW466292 SWANAC21
C 7	14.2	71.0	85	9 CG505735	CG505735 OST54845
C 8	14.2	71.0	98	9 CL529492	CL529492 HIV40D02
C 9	14.2	71.0	98	8 AZ991462	AZ991462 2MD275K09
C 10	14.2	71.0	100	5 BQ856685	BQ856685 QGB5H24.y
C 11	14.2	71.0	100	7 CN870555	CN870555 001204AAO
C 12	14	70.0	85	4 BJ076566	BJ076566 BJ076566
C 13	13.8	69.0	44	8 AZ834300	AZ834300 2M0116D19
C 14	13.8	69.0	55	1 AI569137	AI569137 tr82f12.x
C 15	13.8	69.0	55	1 AU013977	AU013977 AU013977
C 16	13.8	69.0	56	1 AI246108	AI246108 q128h01.x
C 17	13.8	69.0	57	4 BI322307	BI322307 Kx19c11.y
C 18	13.8	69.0	62	1 AI506296	AI506296 VP42a07.x
C 19	13.8	69.0	63	6 CB005039	CB005039 VPC007D11
C 20	13.8	69.0	64	1 AA989601	AA989601 am70b01.s
C 21	13.8	69.0	69	2 AW517453	AW517453 xp94f02.x
C 22	13.8	69.0	69	6 CB912629	CB912629 VDI47F09
C 23	13.8	69.0	71	1 AI472629	AI472629 t178h07.x
C 24	13.8	69.0	71	1 AU259026	AU259026 AU259026

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29	13.8	69.0	75	1 AI431273	AI431273 at57b07.x
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31	13.8	69.0	79	2 BF942148	BF942148 nae87f03.
32	13.8	69.0	80	2 BF942084	BF942084 nae86e07.
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C 40	13.8	69.0	89	1 AA970553	AA970553 oo94h01.8
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ALIGNMENTS

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VERSION AA743605.1 GI:2783111
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 88)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute; Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer

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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 04:59:41 ; Search time 3927 Seconds
(without alignments)
207.910 Million cell updates/sec

Title: US-09-754-468-47

Perfect score: 20

Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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55: /cgn2_6/ptodata/1/pna/US105A_COMB.seq.*
56: /cgn2_6/ptodata/1/pna/US105B_COMB.seq.*
57: /cgn2_6/ptodata/1/pna/US106A_COMB.seq.*
58: /cgn2_6/ptodata/1/pna/US107A_COMB.seq.*
59: /cgn2_6/ptodata/1/pna/US107B_COMB.seq.*
60: /cgn2_6/ptodata/1/pna/US107C_COMB.seq.*
61: /cgn2_6/ptodata/1/pna/US108A_COMB.seq.*
62: /cgn2_6/ptodata/1/pna/US108B_COMB.seq.*
63: /cgn2_6/ptodata/1/pna/US109A_COMB.seq.*
64: /cgn2_6/ptodata/1/pna/US109B_COMB.seq.*
65: /cgn2_6/ptodata/1/pna/US109C_COMB.seq.*
66: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
67: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
68: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
69: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
70: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
71: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
72: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
73: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
74: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
75: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
76: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
77: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
78: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
79: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
80: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
81: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
82: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
83: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
84: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
85: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
86: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
87: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
88: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
89: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
90: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
91: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
92: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
93: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
94: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
95: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
96: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
97: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
98: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
99: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
100: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
101: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
102: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
103: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
104: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
105: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
106: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
107: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
108: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
109: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
110: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
111: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
112: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
113: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
114: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
115: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*
116: /cgn2_6/ptodata/1/pna/US110_COMB.seq.*

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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 04:52:49 ; Search time 3094 Seconds
(without alignments)
246.052 Million cell updates/sec

Title: US-09-754-468-47
Perfect score: 20
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 05:11:41 ; Search time 400 Seconds
(without alignments)
58.914 Million cell updates/sec

Title: US-09-754-468-47
Perfect score: 20
Sequence: 1 gattagcataataaaatctc 20
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5793115 seqs, 589143167 residues

Total number of hits satisfying chosen parameters: 11586230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New.*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
9: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 04:38:33 ; Search time 1670 Seconds
(without alignments)
580.302 Million cell updates/sec

Title: US-09-754-468-47
Perfect score: 20
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 04:03:09 ; Search time 433 Seconds
(without alignments)
273.429 Million cell updates/sec

Title: US-09-754-468-47
Perfect score: 20
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 06:21:46 ; Search time 1662 Seconds
(without alignments)
583.095 Million cell updates/sec

Title: US-09-754-468-47
Perfect score: 20
Sequence: 1 gattagcataataaatctc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 2238514

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description

Mon Mar 28 08:23:20 2005

us-09-754-468-47.sizelim.rni

GenCore version 5.1.6
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QM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 07:34:21 ; Search time 127 Seconds
(without alignments)
257.681 Million cell updates/sec

Title: US-09-754-468-47
Perfect score: 20
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1330268

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: March 26, 2005, 06:19:36 ; Search time 422 Seconds
(without alignments)
280.556 Million cell updates/sec

Title: US-09-754-468-47
Perfect score: 20
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4530610

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N Geneseq_16Dec04:*
- 1: Geneseqn1980s:*
 - 2: Geneseqn1990s:*
 - 3: Geneseqn2000s:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
 - 6: Geneseqn2002as:*
 - 7: Geneseqn2002bs:*
 - 8: Geneseqn2003as:*
 - 9: Geneseqn2003bs:*
 - 10: Geneseqn2003cs:*
 - 11: Geneseqn2003ds:*
 - 12: Geneseqn2004as:*
 - 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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Mon Mar 28 08:23:20 2005

us-09-754-468-47.sizelim.rnpn

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 07:50:07 ; Search time 396 Seconds
(without alignments)
59.509 Million cell updates/sec

Title: US-09-754-468-47
Perfect score: 20
Sequence: 1 gattagcataataaatctc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5793115 seqs, 589143167 residues

Total number of hits satisfying chosen parameters: 10729062

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA_New.*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
9: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 05:27:46 ; Search time 499 Seconds
(without alignments)
238.851 Million cell updates/sec

Title: US-09-754-468-47
Perfect score: 20
Sequence: 1 gattagcataataaaatctc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 04:55:19 ; Search time 129 Seconds
(without alignments)
253.686 Million cell updates/sec

Title: US-09-754-468-47
Perfect score: 20
Sequence: 1 gattagcataataaaatctc 20
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 08:17:57 ; Search time 489 Seconds
(without alignments)
243.735 Million cell updates/sec

Title: US-09-754-468-47
Perfect score: 20
Sequence: 1 gattagcataataaatctc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 5451806

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES